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TITLE: A MAMMALIAN MUCINASE, ITS RECOMBINANT  
PRODUCTION, AND ITS USE IN THERAPY OR  
PROPHYLAXIS AGAINST DISEASES IN WHICH MUCUS IS  
INVOLVED OR INFECTION DISEASES

Inventor: Aerts et al.  
Serial No. 10/004,219

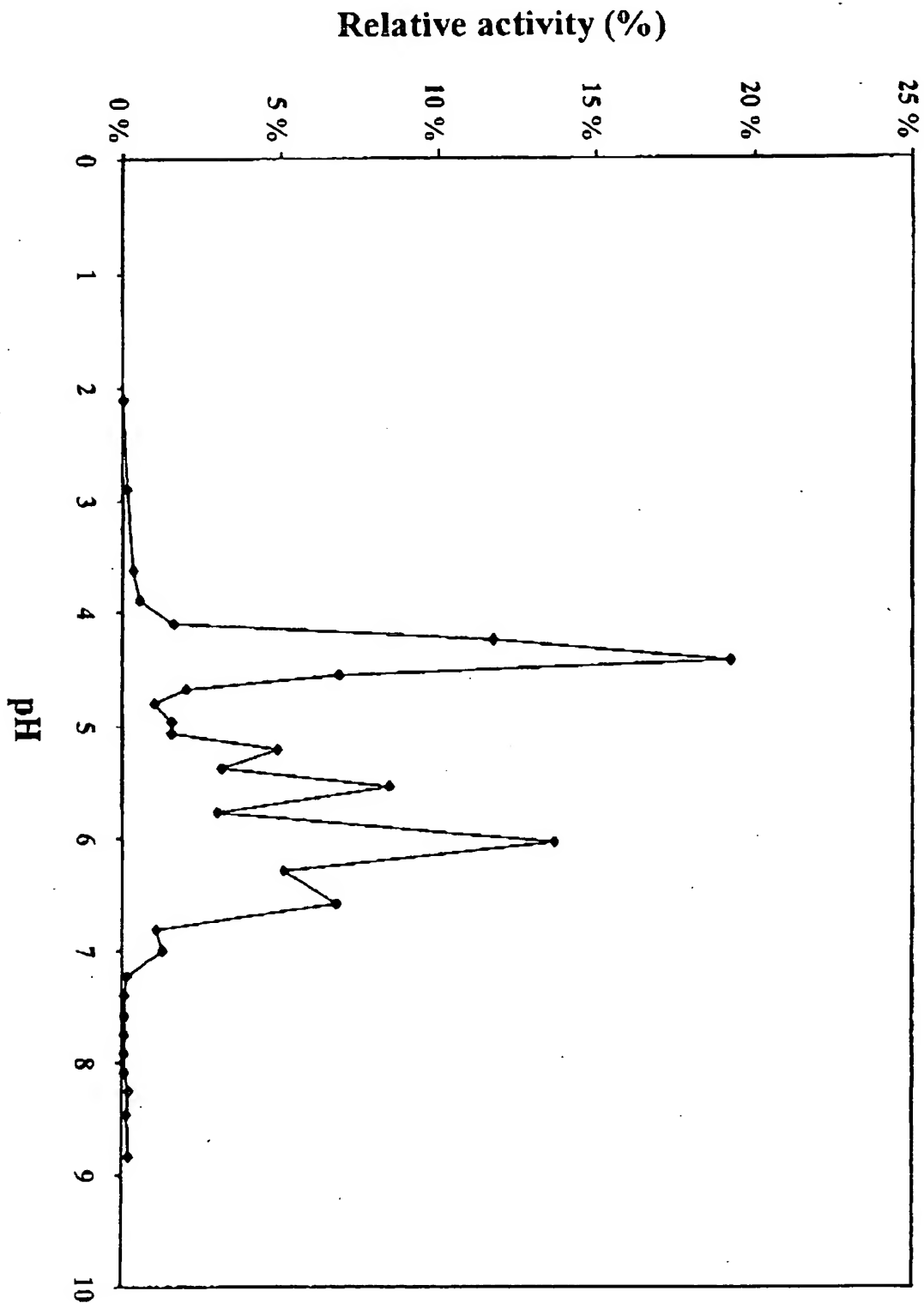


Figure 1

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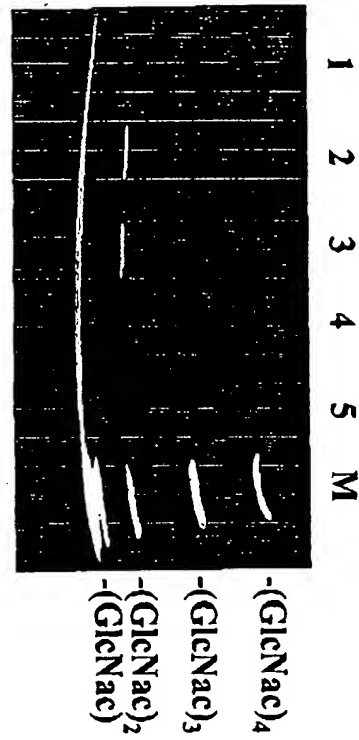


Figure 2

TITLE: A MAMMALIAN MUCINASE, ITS RECOMBINANT  
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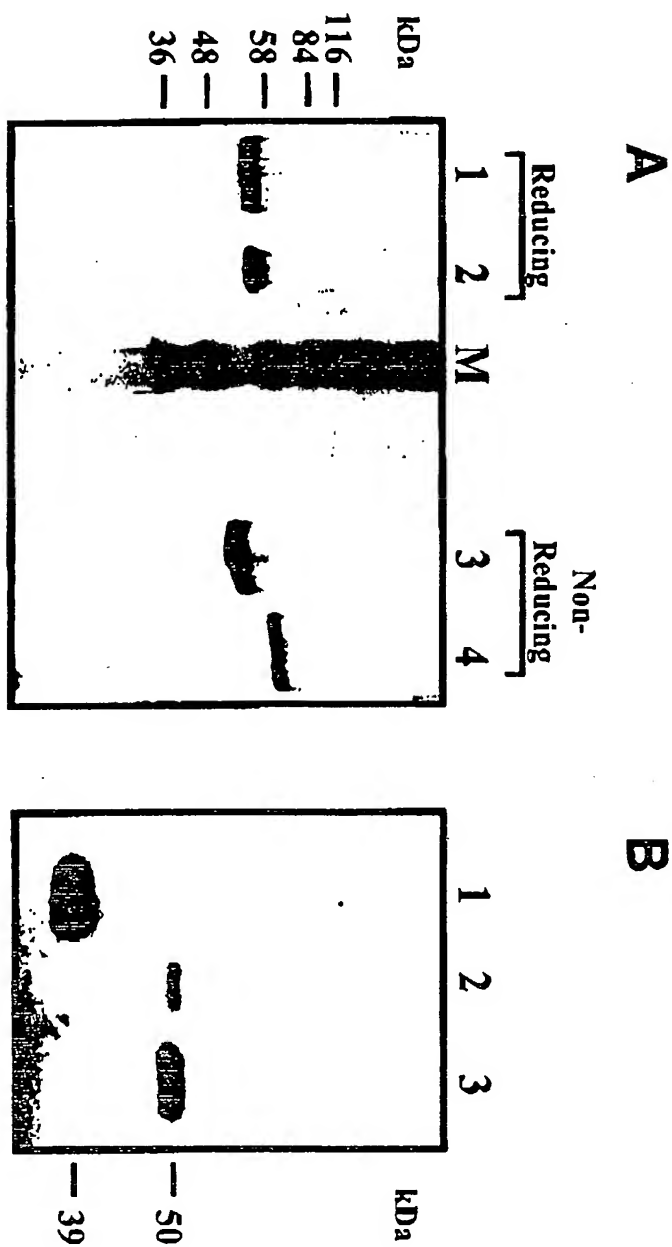
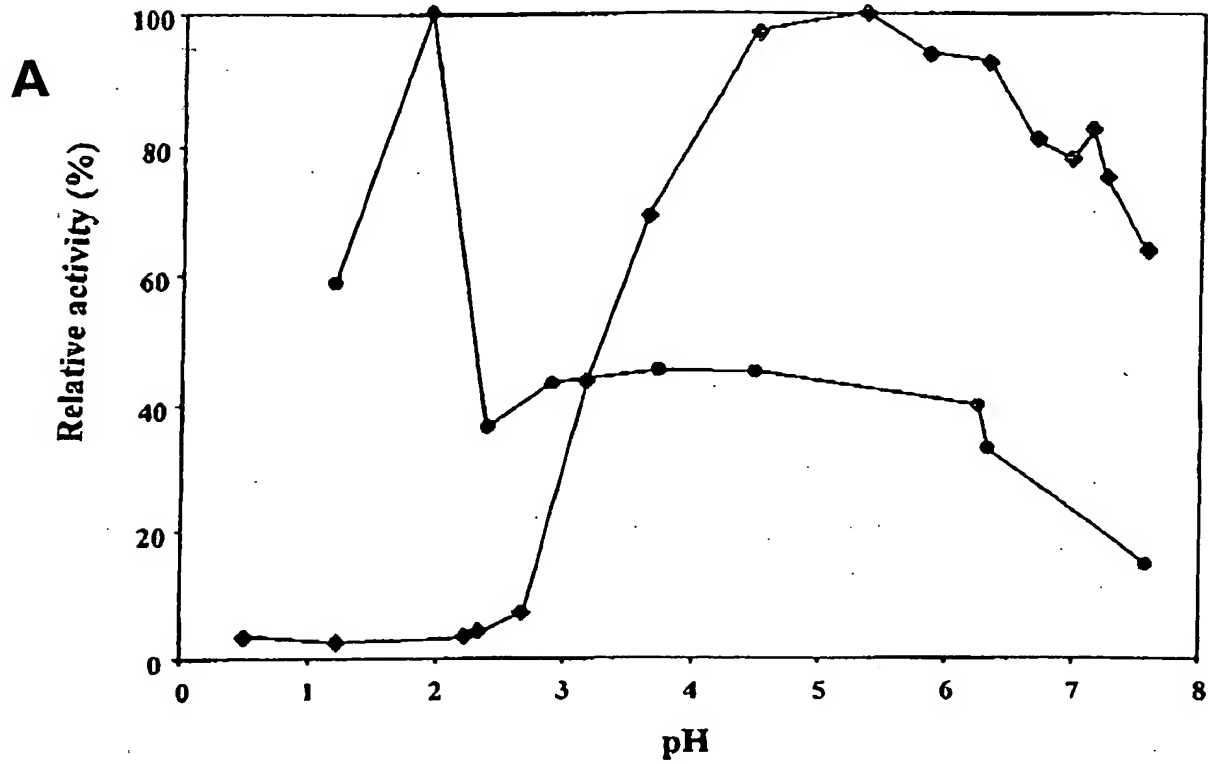


Figure 3

Figure 4

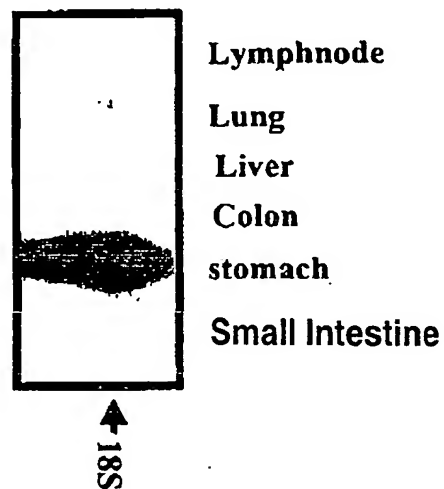
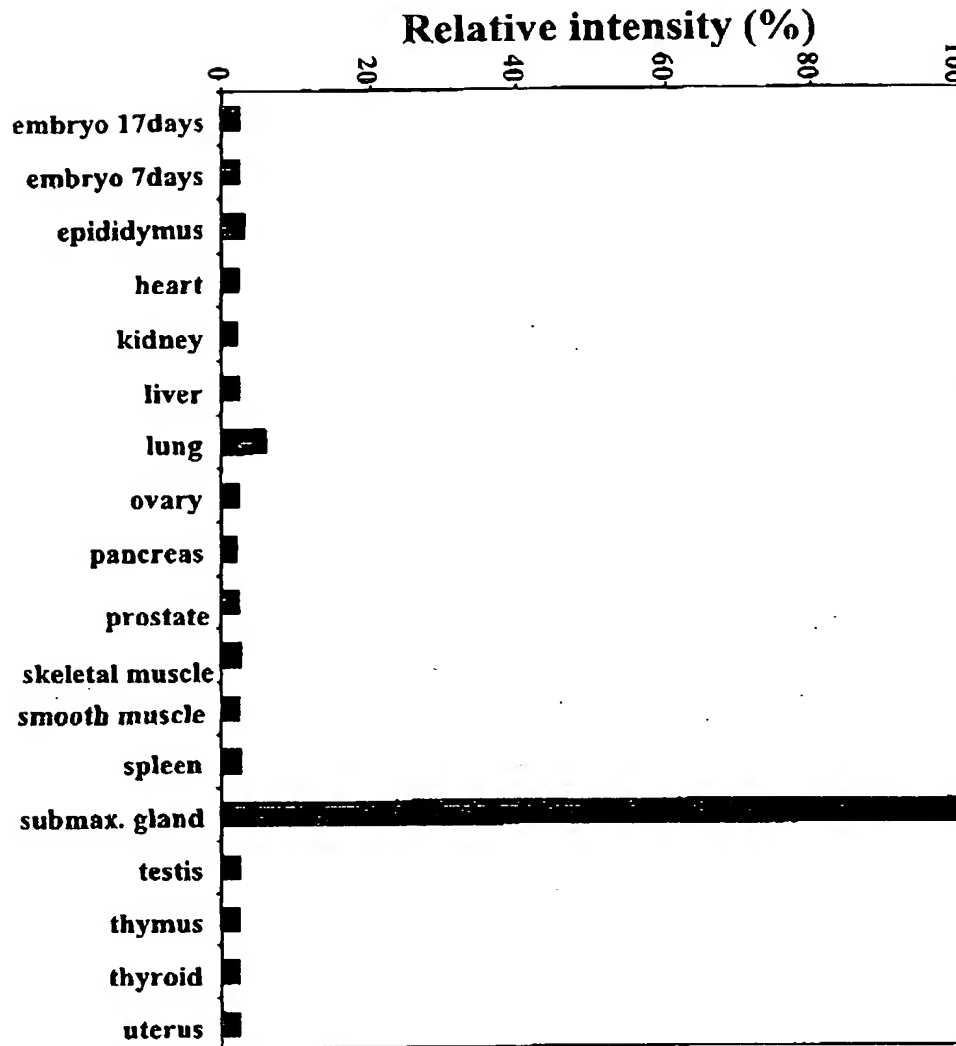


**B**

	pH2	pH7
h-chitotriosidase	0%	100%
m-AMCase	108%	98%

**C**

TCA(%)	0.5	1.25	2.5	5.0
h-chitotriosidase	58%	74%	97%	100%
m-AMCase	0%	8%	74%	100%



**A**

**B**

**Figure 5**

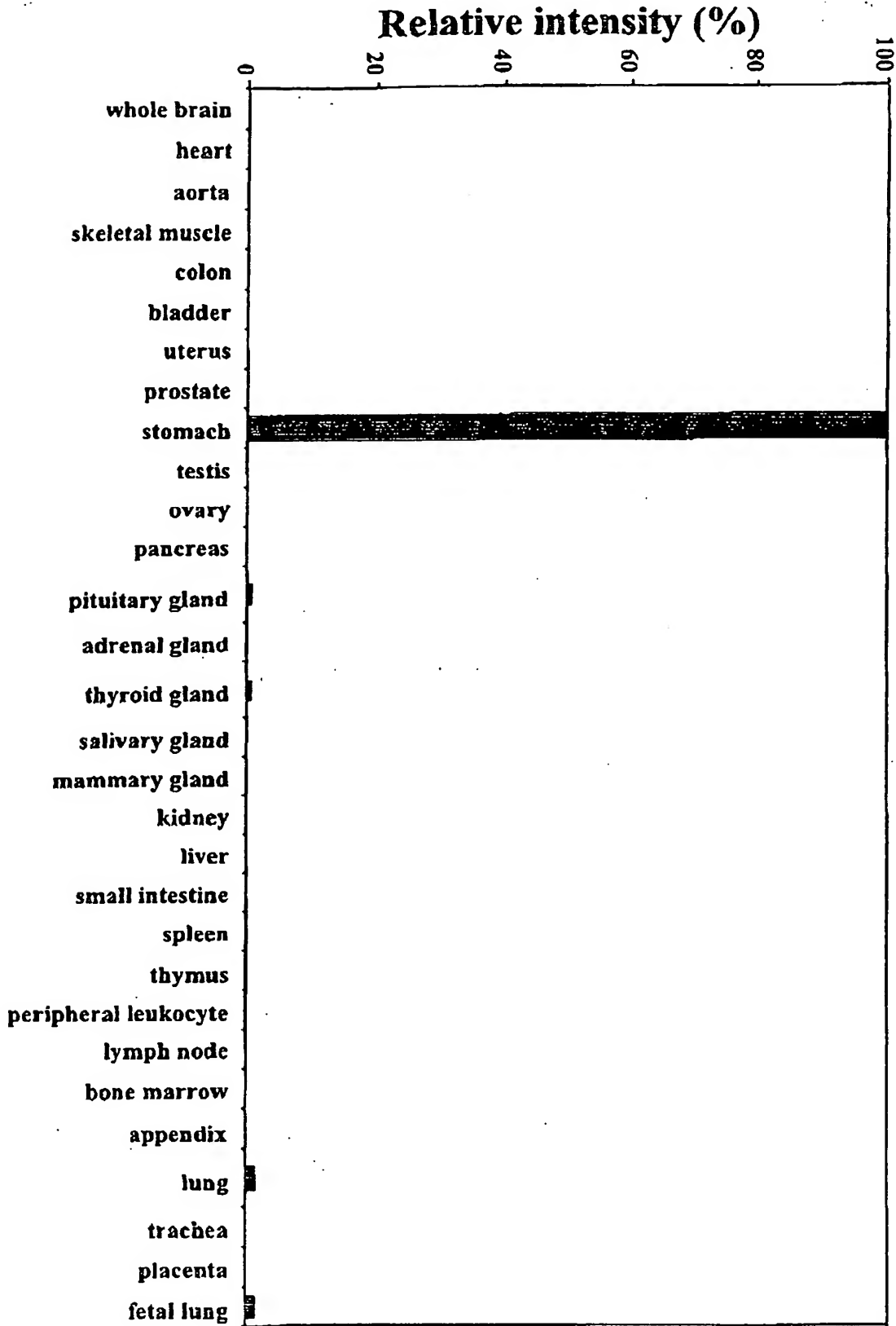


Figure 6

Figure 7





Figure 8. From top to bottom: amino acid sequence (m) AMCase (SEQ ID NO:9), (h) AMCase (SEQ ID NO:14) and (h) chitotriosidase (SEQ ID NO:10). Residues conserved among at least two out of the three sequences are in bold.

1 YNLICYFTNWAQYRPGLGSFKPDDINPCLCTHLIYAFAGMQNN 43  
1 YQLTCYFTNWAQYRPGLGRFMPDNIDPCLCTHLIYAFAGRQNN 43  
1 AKLVCYFTNWAQYRQGEARFLPKDLDPCLCTHLIYAFAGMTNH 43

44 EITTIEWNDVTLYKAFNDLKNRNSKLKTLLAIGGWNFGTAPF 85  
44 EITTIEWNDVTLYQAFNGLKNKNSQLKTLLAIGGWNFGTAPF 85  
44 QLSTTEWNETLYQEFNGLKKMNPCLKTLLAIGGWNFGTQKF 85

86 TTMVSTSQNRQTFITSVIKFLRQYGF DGLDL DWEYPGSRGSP 128  
86 TAMVSTPENRQTFITSVIKFLRQYEF DGLDF DWEYPGSRGSP 128  
86 TDMVATANNRQTFVNSAIRFLRKYSF DGLDL DWEYPGSQGS 128

129 QDKHLFTVLVKEMREAFEQEAIENRPRMLMVTA AVAGGISNIQ 171  
129 QDKHLFTVLVQEMREAFEQEAKQINKPRMLMVTA AVAAGISNIQ 171  
129 VDKERFTTLVQDLANAFQQAQTSGKERLLLSAAVPAGQTYVD 171

172 AGYEIPELSKYLD F I H V M T Y D L H G S W E G Y T G E N S P L Y K Y P T E 213  
172 SGYEIPQLSQYLDYIHVMTYDLHGSWEGYTGENSPLYKYPTD 213  
172 AGYEVDKIAQNLD F V N L M A Y D F H G S W E K V T G H N S P L Y K R Q E E 213

214 TGSNAYLNVDYVMNYWKNNGAPAEKLIVGFPEYGH T F I L R N P S 256  
214 TGSNAYLNVDYVMNYWKDNGAPAEKLIVGFPTYGHNFILSNPS 256  
214 SGAAASLNVDAAVQQWLQKGT PASKLILGMPTYGRSFTLASSS 256

257 DNGIGAPTSGDG P A G A Y T R Q A G F W A Y Y E I C T F L R S G A T E V W D A 299  
257 NTGIGAPTSGAG P A G P Y A K E S G I W A Y Y E I C T F L K N G A T Q G W D A 299  
257 DTRVGAPATGSGTPGPFTKEGGMLAYYEVCSW - -KGATKQRIQ 297

300 SQEVPYAYKAN E W L G Y D N I K S F S V K A Q W L K Q N N F G G A M I W A I D 342  
300 PQEVPYAYQGNVWVG Y D N I K S F D I K A Q W L K H N K F G G A M V W A I D 342  
300 QVPYIFRDNQWVGFD D V E S F K T K V S Y L K Q K G L G G A M V W A L D 340

343 LDDFTGSFCDQ G K F P L T S T L N K A L G I S T E G C T A P D V P S E P V T T - 385  
343 LDDFTGTFCNQG K F P L I S T L K K A L G L Q S A S C T A P A Q P I E P I T A A 386  
341 LDDFAGFSCNQGRYPLIQTLRQELSLPYLPSGTPEL-EVPKPGQ 383

386 - -PPGSGSGGGSSGGSSGGSGGFCADKADGLYPVADDRNAFWQC 426  
387 PSGSGNGSGSSSSGGSSGGSGGFCAVRANGLYPVANNRNAFWHC 429  
384 PS - - - - -EPEHG P S P G Q D T F C Q G K A D G L Y P N P R E R S S F Y S C 419

INGITYQQHCQAGLVFD T S C N C C N W P 452  
VNGVTYQQNCQAGLVFD T S C D C C N W A 455  
AAGRLFQQSCPTGLVFSNSCKCCTWN 445